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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/088,187	09/25/2002	Caroline Dean	0380-P02825USO	8783

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EXAMINER	
BAUM, STUART F	

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 03/14/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/088,187	DEAN ET AL.	
	Examiner	Art Unit	
	Stuart F. Baum	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *06 December 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-34* is/are pending in the application.

4a) Of the above claim(s) *4,7,9-15,25-29,33 and 34* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-3,5,6,8,16-24 and 30-32* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *25 September 2002* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *10/21/2002*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

1. Claims 1-34 are pending.

2. Applicant's election with traverse of Group I, claims 1-8, 16-24, 30-32 to the extent they are directed to SEQ ID NO:10 encoding SEQ ID NO:11 in the reply filed on 12/6/2004 is acknowledged. The traversal is on the ground(s) that the restriction requirement is improper for failure to comply with the relevant provisions of the MPEP pertaining to unity of invention determinations (page 14, 1st full paragraph).

This is not found persuasive because the office contends that a lack of unity was required according to relevant provisions of the MPEP.

Applicants contend that during the international stage of this application, the Examiner did not make a lack of unity finding (paragraph bridging pages 14-15).

This is not found persuasive because the office is not bound by lack of unity practice that was done in a PCT.

Applicants contend that Groups I through VI possess a corresponding special technical feature and that the Finnegan et al reference does not teach a VRN1 nucleotide sequence that is capable of altering the vernalisation response of a plant into which the nucleic acid is introduced, based on Applicants' definition of a VRN1 in terms of specific sequences and variants, see, e.g., pages 2-18 of specification (page 15, 2nd full paragraph). Applicants contend that claims 2-7, 9-15, 26-29 and 33 recite specific amino acid or nucleotide sequences which Finnegan et al do not teach.

This is not found persuasive because Applicants' claim 1 recites " a VRN1 nucleotide sequence encoding a polypeptide which is capable of specifically altering the vernalisation

response...". The Office contends that the modifier "which" is modifying the noun 'VRN1 nucleotide sequence' and not the noun 'polypeptide'. The office also contends that Applicants define "VRN1" to encompass functional variants (page 18, lines 28-30 of Applicants' specification) and Applicants further define "functional variants" to include variants which comprise only a fragment corresponding to a portion of the sequence provided (page 8, lines 16-20). The office interprets a fragment to read on a codon of Applicants' sequence and the sequence of Finnegan et al when transformed into a plant affects the vernalization requirement of said plant. Given the Office's interpretation of the claim as discussed above, and Applicants' broad definition of 'VRN1', the sequence disclosed by Finnegan et al comprises a fragment of Applicants sequence and can be used to alter the vernalisation response of a plant when the nucleic acid is introduced and expressed in a plant. And lastly, the office contends that the special technical feature is assessed according to the first claimed invention.

Applicants contend that the VRN1 nucleotide and amino acid sequences i.e., SEQ ID NO:10 and 11, are unified by a common inventive concept (page 16, 1st full paragraph). Applicants refer to Example 17 of Annex B, Part 2 of the PCT Administrative Instructions as amended 01 July 1992.

This is not found persuasive because the office contends that the special technical feature is assessed according to the first claimed invention which recites "a VRN1 nucleotide sequence" and does not specify that the VRN1 nucleotide sequence is set forth in SEQ ID NO:10. Example 17 of Annex B, Part 2 of the PCT Administrative Instructions is directed toward a particular SEQ ID NO encoding a specific amino acid sequence. Applicants' claim 1 is drawn to many nucleic

acid sequences encoding many different proteins based on Applicants' definition of "VRN1" as discussed above.

Applicants contend that even if the restriction requirement is not withdrawn for Groups I through VI, Applicants urge at least a modified restriction requirement wherein Groups I, III, V, and VI are rejoined according to PCT Administrative Instructions, Appendix AI, Annex B, Part 1 (page 16, bottom paragraph and paragraph bridging pages 16-17). Applicants contend that it is clear that the special technical feature which links the claims of Groups I, II, V, and VI, i.e., the isolated VRN1 nucleic acid, defines a contribution over the prior art and this feature is embodied as an essential feature of all of the Groups defined by the Examiner (page 17, bottom paragraph). Applicants contend that Group III should be rejoined with Group I because it relates to a method for producing a nucleic acid molecule of the instant application (page 18, 1st full paragraph). Applicants contend that Groups V and VI should be rejoined because Group V recites the same special technical feature and Group VI is the promoter of the VRN1 gene and is part of the isolated VRN1 nucleic acid molecule.

This is not found persuasive because Applicants' special technical feature of a VRN1 nucleotide sequence is taught in the prior art as discussed above. The claims are not linked by a single technical feature because they are each drawn to products and processes not shared by the other. The isolated nucleic acid and transgenic host cell and plant and methods comprising said nucleic acid of Group I, is not shared by the probe or primer of Group II, which is not shared by the process for producing a nucleic acid of Group III, which is not shared by the method for increasing vernalization requirement of a plant comprising antisense, co-suppression or ribozyme of Group V or which is not shared by the promoter of Group VI. In addition, claim 11 of Group

III is drawn to a process for producing a nucleic acid comprising the VRN1 nucleotide sequence encoding a derivative polypeptide of SEQ ID NO:11 by way of addition, insertion, deletion or substitution of one or more amino acids. This claim reads on a process for producing any polypeptide, which does not share a technical feature of claim 1 from Group I.

Lastly, Applicants contend that by dividing this application into six separate patent applications, Applicants will be unduly and unfairly burdened with excessive fees and cost associated with the prosecution and maintenance of multiple patents (page 18, 2nd full paragraph).

This is not found persuasive because Applicants' financial concerns are not a consideration during restriction practice.

The requirement is still deemed proper and is therefore made FINAL.

Claims 4, 7, 9-15, 25-29, and 33-34 are withdrawn from consideration because they are drawn to non-elected inventions.

3. Claims 1-3, 5-6, 8, 16-24, 30-32 are examined in the present office action.

Specification

4. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See for example page 39, lines 26 and 32; page 42, lines 3,5,10-12; page 44, line 18; page 48, line 7; page 56, line 22. See MPEP § 608.01.

Claim Objections

5. Claim 24 is objected to for not reciting the article "a" before the word "propagule".

Written Description

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

6. Claims 1-3, 5-6, 8, 16-24, and 30-32 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claims are drawn to an isolated nucleic acid molecule which comprises a VRN1 nucleotide sequence encoding a polypeptide which is capable of specifically altering the vernalization response of a plant or complement thereof, a recombinant vector comprising said nucleic acid molecule, a method for transforming a host cell or plant comprising said vector, or plant transformed therewith, or method for influencing or affecting the vernalisation phenotype of a plant comprising said nucleic acid; or a degeneratively equivalent sequence of nucleotides 269-1295 of SEQ ID NO:10, or wherein the nucleotide sequence encodes a variant resistance polypeptide which is a homologous variant of SEQ ID NO:11 and which shares at least about 50%, 60%, 70%, 80% or 90% identity therewith, or wherein the nucleotide sequence encodes a

derivative polypeptide of SEQ ID NO:11 by way of addition, insertion, deletion, or substitution of one or more amino acids, or wherein the nucleotide sequence consists of an allelic or other homologous variant of nucleotides 269-1295 inclusive of SEQ ID NO:10 or a sequence which is degeneratively equivalent thereto.

Applicants disclose a putative VRN1 nucleic acid sequence of SEQ ID NO:10 encoding the polypeptide of SEQ ID NO:11 (page 36, Brief Description of the Drawings for Figure 7). Applicants identified the VRN1 nucleic acid by first isolating vrn1 mutants. The vrn1 mutation was selected from mutagenized populations of Arabidopsis fca-1 plants on the basis of its impairment of the acceleration of flowering following a six week cold treatment (pages 36-37, Example 1). The VRN1 nucleic acid sequence of SEQ ID NO:10 was cloned using a map based approach and was found to complement the vrn1 phenotype (pages 38-42, Examples 3-6). Applicants disclose that the putative protein of SEQ ID NO:11 comprises two regions which are related to B3 domains and a region which lies between the two B3 domains is not obviously related to any domain of known function (page 46-48 of Example 8).

The Applicants do not identify essential regions of any VRN1 nucleotide sequence encoding any polypeptide which is capable of specifically altering the vernalization response of a plant. Applicants also do not identify essential regions of a VRN1 polypeptide of SEQ ID NO:11 encoded by nucleotides 269-1295 of SEQ ID NO:10 nor proteins that exhibit at least about 50%, 60%, 70%, 80%, or 90% identity with SEQ ID NO:11 nor derivative polypeptides of SEQ ID NO:11 that comprise addition, insertion, deletion or substitution of one or more amino acids nor allelic or other homolgous variants of nucleotides 269-1295 of SEQ ID NO:10, nor a

degeneratively equivalent sequence of nucleotides 269-1295 of SEQ ID NO:10 that all of which encode a protein with the same activity as the protein of SEQ ID NO:11.

The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. See University of California v. Eli Lilly and Co., 119 F.3d 1559, 1568, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). In summary, the court stated that a written description of an invention requires a precise definition, one that defines the structural features of the chemical genus that distinguishes it from other chemical structures. A definition by function does not suffice to define the genus because it is only an indication of what the gene does, rather than what it is. The court goes on to say, "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

Applicants fail to describe a representative number of polynucleotide sequences encoding a VRN1 protein falling within the scope of the claimed genus of VRN1 polypeptides or polypeptides which exhibit 50%, 60%, 70%, 80% or 90% identity to SEQ ID NO:11, or encode derivative polypeptides of SEQ ID NO:11 by way of addition, insertion, deletion, or substitution of one or more amino acids, or a representative number of sequences that are degeneratively equivalent sequence of nucleotides 269-1295 of SEQ ID NO:10. Applicants only describe a single sequence of SEQ ID NO:10 encoding SEQ ID NO:11. Furthermore, Applicants fail to describe structural features common to members of the claimed genus of polynucleotides.

Hence, Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*. Furthermore, given the lack of description of the necessary elements essential for the VRN1 protein of SEQ ID NO:11, it remains unclear what features identify an Arabidopsis VRN1 protein of SEQ ID NO:11. Since the genus of VRN1 proteins of SEQ ID NO:11 has not been described by specific structural features, the specification fails to provide an adequate written description to support the breath of the claims.

Enablement

7. Claims 1-3, 5-6, 8, 16-24, 30-32 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The claimed invention is not supported by an enabling disclosure taking into account the *Wands* factors. *In re Wands,* 858/F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988). *In re Wands* lists a number of factors for determining whether or not undue experimentation would be required by one skilled in the art to make and/or use the invention. These factors are: the quantity of experimentation necessary, the amount of direction or guidance presented, the presence or absence of working examples of the invention, the nature of the invention, the state of the prior art, the relative skill of those in the art, the predictability or unpredictability of the art, and the breadth of the claim.

The claims are drawn to an isolated nucleic acid molecule which comprises a VRN1 nucleotide sequence encoding a polypeptide which is capable of specifically altering the

vernalization response of a plant or complement thereof, a recombinant vector comprising said nucleic acid molecule, a method for transforming a host cell or plant comprising said vector, or plant transformed therewith, or method for influencing or affecting the vernalisation phenotype of a plant comprising said nucleic acid; for wherein the VRN1 nucleotide sequence is from nucleotides 269-1295 of SEQ ID NO:10 or degeneratively equivalent sequences thereof, or wherein the nucleotide sequence encodes a variant resistance polypeptide which is a homologous variant of SEQ ID NO:11 and which shares at least about 50%, 60%, 70%, 80% or 90% identity therewith, or wherein the nucleotide sequence encodes a derivative polypeptide of SEQ ID NO:11 by way of addition, insertion, deletion, or substitution of one or more amino acids, or wherein the nucleotide sequence consists of an allelic or other homologous variant of nucleotides 269-1295 inclusive of SEQ ID NO:10.

Applicants define "VRN1" as intending to cover any of the nucleic acids that are described in the text of the specification (page 18, lines 29-30). The specification discloses that "a variant polypeptide encoded by a nucleic acid of the present invention may include within the sequence shown in Fig 7, a single amino acid or ... about 40 or 50 changes, or greater that about 50, 60, 70, 80, or 90 changes" (page 9, lines 16-20). In addition, Applicants also state "Alternatively, changes to a sequence may produce a derivative by way of one or more of addition, insertion, deletion or substitution of one or more nucleotides in the nucleic acid, leading to the addition, insertion, deletion or substitution of one or more amino acids in the encoded polypeptide" (page 9, lines 31-35). Based on Applicants definition as stated above, the Office interprets "VRN1 nucleotide sequence" to read on any nucleotide sequence.

Applicants disclose a putative VRN1 nucleic acid sequence of SEQ ID NO:10 encoding the polypeptide of SEQ ID NO:11 (page 36, Brief Description of the Drawings for Figure 7). Applicants identified the VRN1 nucleic acid by first isolating *vrn1* mutants. The *vrn1* mutation was selected from mutagenized populations of Arabidopsis *fca-1* plants on the basis of its impairment of the acceleration of flowering following a six week cold treatment (pages 36-37, Example 1). The VRN1 nucleic acid sequence of SEQ ID NO:10 was cloned using a map based approach and was found to complement the vrn1 phenotype (pages 38-42, Examples 3-6). Applicants disclose that the putative protein of SEQ ID NO:11 comprises two regions which are related to B3 domains and a region which lies between the two B3 domains is not obviously related to any domain of known function (page 46-48 of Example 8).

Applicants have not reduced to practice the invention. The specification fails to provide guidance for one of skill in the art how to make and/or use the claimed invention. Applicants have not transformed a wild-type plant with any of the claimed sequences to produce a plant with an altered vernalization phenotype. Applicants have only taught that the isolated nucleic acid sequence of SEQ ID NO:10 can complement the *vrn1* mutant phenotype in a *fca-1* mutant background (paragraph bridging pages 40-41). Applicants isolated the VRN1 nucleic acid sequence of SEQ ID NO:10 on the basis of a mutant plant in which the endogenous VRN1 nucleic acid sequence of SEQ ID NO:10 was mutant, thereby producing a mutant phenotype of delayed flowering. Applicants have not taught how one skilled in the art can use the claimed sequences to generate a plant with an altered vernalisation phenotype, without having to do additional undue experimentation in order to achieve the desired results. In addition, Applicants

have not taught how one skilled in the art would use a plant transformed with any of the claimed sequences.

Transforming plants with heterologous genes that are involved in plant development produce unpredictable results. Kano-Murakami et al (1993, FEBS 334:365-368) teach introducing the *Oryza sativa* homeobox 1 (OSH1) gene into tobacco. OSH1 is a rice homologue of the *Knotted-1* homeobox gene from maize. Kano-Murakami et al teach transgenic tobacco plants comprising the OSH1 gene display a "range of phenotypes which include abnormalities in leaf and petal shape as well as stem height and number" (page 365, right column, 1st paragraph).

The state-of-the-art is such that one of skill in the art cannot predict which nucleic acids that are 50% sequence identical to SEQ ID NO:11 will encode a protein with the same activity as the protein of SEQ ID NO:11. The prediction of protein structure from sequence data and, in turn, utilizing predicted structural determinations to ascertain functional aspects of the protein, is extremely complex, and the positions within the protein's sequence where amino acid substitutions can be made with a reasonable expectation of maintaining function are limited (Bowie et al, Science 247:1306-1310, 1990, see especially page 1306). Proteins may be sensitive to alterations in even a single amino acid in a sequence. For example, the replacement of a glycine residue located within the START domain of either the PHABULOSA or PHAVOLUTA protein receptor with either an alanine or aspartic acid residue, alters the sterol/lipid binding domain (McConnell et al, Nature 411 (6838):709-713, 2001, see especially page 710, left column, 2nd paragraph).

Applicants have not disclosed how one makes or isolates any of the sequences that are encompassed by Applicants' broad claims. Applicants have not taught which regions of the

respective polynucleotides can be used to amplify any of said polynucleotides or which regions can be used as a probe to isolate any of said polynucleotide sequences.

In the absence of guidance, undue trial and error experimentation would be required for one of ordinary skill in the art to screen through the multitude of non-exemplified sequences, either by using non-disclosed fragments of SEQ ID NO:10 as probes or by designing primers to undisclosed regions of SEQ ID NO:11 and isolating or amplifying fragments, subcloning the fragments, producing expression vectors and transforming plants therewith, or because of Applicants broad definition of a "VRN1 nucleotide sequence" as discussed above, amplifying any sequence from any plant and subcloning said sequence into an expression vector and transforming plants, in order to identify those, if any, that when over-expressed in a plant, produce an altered vernalisation phenotype.

Therefore, given the breadth of the claims; the lack of guidance and examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue experimentation would be required to practice the claimed invention, and therefore the invention is not enabled.

Even if Applicant is able to overcome the issues set forth above, Applicant is still limited to nucleotides 269-1295 of SEQ ID NO:10 encoding SEQ ID NO:11.

Claim Rejections - 35 USC § 102

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

8. Claims 1, 3, 5-6, 8, 16-22, and 30-32 are rejected under 35 U.S.C. 102(b) as being anticipated by Kamada et al (1992, Plant Tissue Culture Letters 9(3):206-208).

The claims are drawn to an isolated nucleic acid molecule which comprises a VRN1 nucleotide sequence encoding a polypeptide which is capable of specifically altering the vernalization response of a plant or complement thereof, or wherein the nucleic acid encodes a derivative of the polypeptide of SEQ ID NO:11 by way of addition, insertion, deletion or substitution of one or more amino acids, or wherein the nucleic acid sequence is a degeneratively equivalent sequence of the sequence of nucleotides 269-1295 of SEQ ID NO:10, or wherein the nucleic acid consists of a allelic or other homologous variant, a recombinant vector comprising said nucleic acid molecule, or wherein the nucleic acid is operably linked to a promoter for transcription in a host cell, or wherein said vector is a plant vector, a method for transforming a host cell or plant comprising said vector, or plant transformed therewith, or method for influencing or affecting the vernalisation phenotype of a plant comprising expression of said nucleic acid, or wherein said method modifies the kinetics of the vernalisation response such as to alter the phenotype with respect to length of a vernalization period.

Applicants define "VRN1" as intending to cover any of the nucleic acids that are described in the text of the specification (page 18, lines 29-30). The specification discloses that "a variant polypeptide encoded by a nucleic acid of the present invention may include within the sequence shown in Fig 7, a single amino acid or ... about 40 or 50 changes, or greater that about 50, 60, 70, 80, or 90 changes" (page 9, lines 16-20). In addition, Applicants also state "Alternatively, changes to a sequence may produce a derivative by way of one or more of addition, insertion, deletion or substitution of one or more nucleotides in the nucleic acid, leading to the addition, insertion, deletion or substitution of one or more amino acids in the encoded polypeptide" (page 9, lines 31-35).

Based on Applicants' definition of "VRN1", the Office interprets a "VRN1" nucleotide sequence to read on any nucleotide sequence because Applicants' definition reads on one base pair. Because Applicants do not define "homologous variant", or "degeneratively equivalent" the office interprets "homologous variant" and "degeneratively equivalent" to read on any sequence.

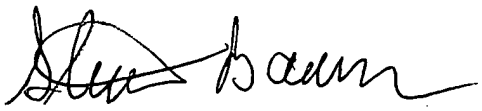
Kamada et al disclose a recombinant plant vector comprising the RolC gene operably linked to a promoter operable in plants and *Agrobacterium* and plant cells transformed therewith, and the regeneration of transformed plant cells into transgenic plants (page 207-208, Material and Methods section). Kamada et al disclose that *Cichorium* plants transformed with the RolC gene showed flower formation without vernalisation (page 212, top paragraph). The teachings of Kamada et al disclose a method for influencing or affecting the vernalisation phenotype of a plant comprising transforming a plant with the RolC gene. The transformed plants of Kamada et al flowered without a vernalization period, therefore the vernalization period was reduced, which signifies that the kinetics of the plant have been modified, and as such, Kamada et al anticipates the claimed invention.

9. No claims are allowed.

10. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Stuart F. Baum whose telephone number is 571-272-0792. The examiner can normally be reached on M-F 8:30-5:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on 571-272-0804. The fax phone number for the organization where this application or proceeding is assigned is (703) 872-9306.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600.



Stuart F. Baum Ph.D.
Patent Examiner
Art Unit 1638
March 3, 2005